Amendments to the Specification:

Please replace the paragraph at page 12, line 27 through page 13, line 1 with the following amended paragraph:

Based on the entire amino acid sequence of KDR protein, twelve types of 9-mer peptides (SEQ ID NOs: 1 to 12), and twelve types of 10-mer peptides (SEQ ID NOs: 13 to 24) were predicted in order from that with the highest binding affinity to HLA-A*2402, using BioInformatics & Molecular Analysis Section (BIMAS) HLA Peptide Binding Prediction software (~~http://~~ on the Worldwide Web at bimas.dcrt.nih.gov/cgi-bin/molbio/ken_parker_comboform) (Table 1). Table 1 shows the binding affinity of each of the 9 mers and 10 mers in order from the highest value, together with the position of their N termini in the amino acid sequence of the KDR protein. In the table, CE652 (SEQ ID NO: 25) refers to one of the epitopes of tumor antigen CEA (carcinoembryonic antigen) that has been reported by Nukaya, I. (Int. J. Cancer 80, 1999). HIV peptides (ILKEPVHGV (SEQ ID NO: 55) and RYLRDQQLL (SEQ ID NO: 56)) were used as the negative control peptides.

Please replace the paragraph at page 17, lines 23-32 with the following amended paragraph:

In a similar manner to Example 1, 15 types of 9-mer peptides (SEQ ID NOs: 26 to 40), and 12 types of 10-mer peptides (SEQ ID NOs: 41 to 52) were predicted from the entire amino acid sequence of the KDR protein, in order from highest binding affinity with HLA-A*0201, using HLA Peptide Binding Prediction software (~~http://~~ on the Worldwide Web at bimas.dcrt.nih.gov/cgi-bin/molbio/ken_parker_comboform) (Table 4). Table 4 shows the binding affinity of each of the 9 mers and 10 mers in order from the highest value, together with the position of their N terminal in the amino acid sequence of the KDR protein. In the table, CEA588 (SEQ ID NO: 53) refers to one of the epitopes of tumor antigen CEA (carcinoembryonic antigen) reported by Tanaka, H. et al. (poster presentation, AACR #3669, vol. 42, p681-682, March 2001).

Please replace the paragraphs at page 21, lines 9-22 with the following amended paragraph:

Homology searches for the peptides of this invention (SEQ ID NO: 2 (amino acid initiation position KDR1318), SEQ ID NO: 3 (KDR220), SEQ ID NO: 5 (KDR189), SEQ ID NO: 8 (KDR169), SEQ ID NO: 11 (KDR826), SEQ ID NO: 30 (KDR773), and SEQ ID NO: 40 (KDR190)) were carried out by using the BLAST program (~~http://www.~~ on the Worldwide Web at ncbi.nlm.nih.gov/blast/blast.cgi). No peptides with a sequence completely identical to any one of these peptides could be found (Table 6). The 9-mer peptide (KDR169) of SEQ ID NO: 8 capable of inducing strong CTL activity in Example 4 had only one sequence containing two mismatches (77.8% homology), and two sequences containing three mismatches (66.7% homology). The peptide of SEQ ID NO: 5 (KDR189), whose remarkable in vivo anti-tumor effect was observed in Example 8, had only one sequence containing three mismatches (66.7% homology).

Table 6 Homology analysis using the BLAST program
(~~http://www.~~ on the Worldwide Web at ncbi.nlm.nih.gov/blast/blast.cgi)